

SEQUENCE LISTING

41

SEQ 1D No.1

5'GTTAGCTCAGATTGAACGCTGGCGGCAGGCTTAAACACATGCAAGTCGAGC
GGTAACAGGGGAGCTTGCTCCTGCTGACGAGCGGCGGACGGGTGAGTAACGC
GTAGGAATCTGCCTAGTAGAGGGGGACAACATGTGGAAACGCATGCTAATAC
CGCATACGCCCTGAGGGGGAAAGGAGGGGACTCTTCGGAGCCTTCCGCTATT
AGATGAGCCTGCGTGAGATTAGCTAGTTGGTAGGGTAAAGGCCTACCAAGGC
GACGATCTCTAACTGGTCTGAGAGGATGACCAGTCACACTGGGACTGAGACA
CGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGC
AAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTAGGGTTGTAAAG
CACTTTCAGGGGTGAGGAAGGGTGATAGGTAAATACGTTATCATCTTGACGTT
AGCCCCAGAAGAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAG
AGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTT
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CTGGCTAGCTAGAGTATGGTAGAGGGGTGTGGAATTTCTGTGTAGCGGTGA
AATGCGTAGATATAGGAAGGAACATCAGTGGCGAAGGCGACACCCTGGACT
AATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACC
CTGGTAGTCCACGCCGTAAACGATGTCTACTAGCCGTTGGGTTGTAATGACTT
AGTGGCGCAGCTAACGCAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAG
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GTGACAAACCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGGCCCTTACG
AGTAGGGCTACACACGTGCTACAATGGCGTATACAGAGGGCTGCAAGCTAGC
GATAGTGAGCGAATCCCACAAAGTACGTCGTAGTCCGGATTGGAGTCTGCAA
CTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGTCACGG
TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGAT
TGCTCCAGAAGTAGCTAGCTTAACCCTTCGGGATGGCGGTTACCACGGAGTG
GTCAATGACTGGGGTTGAAGTCTACGCG-3

SEQ 1D No.2

1 5'GCCCTTGCTC AGATTGAACG CTGGCGGCAG GCCTAACACA TGCAAGTCGA
51 GCGGTAGAGA GAAGCTTGCT TCTCTTGAGA GCGGCGGACG GGTGAGTAAT
101 GCCTAGGAAT CTGCCTGGTA GTGGGGGATA ACGTTCGGAA ACGGACGCTA
151 ATACCGCATA CGTCCTACGG GAGAAAGCAG GGGACCTTCG GGCCTTGCGC
201 TATCAGATGA GCCTAGGTCG GATTAGCTAG TTGGTGAGGT AATGGCTCAC
251 CAAGGCGACG ATCCGTA ACT GGTCTGAGAG GATGATCAGT CACACTGGAA
301 CTGAGACACG GTCCAGACTC CTACGGGAGG CAGCAGTGGG GAATATTGGA
351 CAATGGGCGA AAGCCTGATC CAGCCATGCC GCGTGTGTGA AGAAGGTCTT
401 CGGATTGTAA AGCACTTTAA GTTGGGAGGA AGGGTTGTAG ATTAATACTC
451 TGCAATTTTG ACGTTACCGA CAGAATAAGC ACCGGCTAAC TCTGTGCCAG
501 CAGCCGCGGT AATACAGAGG GTGCAAGCGT TAATCGGAAT TACTGGGCGT
551 AAAGCGCGCG TAGGTGGTTT GTTAAGTTGG ATGTGAAATC CCCGGGCTCA
601 ACCTGGGAAC TGCATTCAA ACTGACTGAC TAGAGTATGG TAGAGGGTGG
651 TGGAATTTCC TGTGTAGCGG TGAAATGCGT AGATATAGGA AGGAACACCA
701 GTGGCGAAGG CGACCACCTG GACTAATACT GACACTGAGG TGCGAAAGCG
751 TGGGGAGCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG
801 TCAACTAGCC GTTGGAAGCC TTGAGCTTTT AGTGGCGCAG CTAACGCATT
851 AAGTTGACCG CCTGGGGAGT ACGGCCGCAA GGTTAAAACT CAAATGAATT
901 GACGGGGGCC CGCACAAGCG GTGGAGCATG TGGTTTAATT CGAAGCAACG
951 CGAAGAACCT TACCAGGCCT TGACATCAA TGAACCTTCT AGAGATAGAT
1001 TGGTGCCCTC GGAACATTG AGACAGGTGC TGCATGGCTG TCGTCAGCTC
1051 GTGTTGTGAA ATGTAAGGGC-3'